J. HINES
306780

```
=> fil medl,caplus,biosis,embase,wpids

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=> s nucleic acid and bound polypeptide

L1             4 FILE MEDLINE
L2             3 FILE CAPLUS
L3             1 FILE BIOSIS
L4             1 FILE EMBASE
L5             2 FILE WPIDS

TOTAL FOR ALL FILES
L6            11 NUCLEIC ACID AND BOUND POLYPEPTIDE

=> dup rem l6

PROCESSING COMPLETED FOR L6
L7             8 DUP REM L6 (3 DUPLICATES REMOVED)

=> d tot all;s nucleic acid bind? motif?


L7   ANSWER 1 OF 8  CAPLUS  COPYRIGHT 1999 ACS          DUPLICATE 1
AN   1997:732139  CAPLUS
DN   128:32121
TI   Nucleic acid-bound polypeptide,
     method of producing nucleic acid-bound
     polypeptide, and immunoassay using the polypeptide
IN   Takemura, Fuminori; Ueno, Eiichi; Itoh, Satoru
PA   Fujirebio Inc., Japan
SO   Eur. Pat. Appl., 38 pp.
     CODEN: EPXXDW
DT   Patent
LA   English
IC   ICM  C07K002-00
     ICS  C12N015-62; G01N033-53
CC   9-10 (Biochemical Methods)
     Section cross-reference(s): 3, 15
FAN.CNT 1
     PATENT NO.         KIND  DATE          APPLICATION NO.   DATE
     ---------------    ----  --------      ---------------   --------
PI   EP 805160           A1   19971105      EP 1997-400985    19970430
```

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

JP 10081698 A2 19980331 JP 1997-121803 19970424
AU 9719978 A1 19971204 AU 1997-19978 19970430

PRAI JP 1996-134444 19960501

AB A **nucleic acid-bound polypeptide** produced by binding a **nucleic acid** to a polypeptide, a method of producing the **nucleic acid-bound polypeptide**, and applications of the **nucleic acid-bound polypeptide**, including immunoassays for an antigen or antibody, such as an agglutination immunoassay are provided. Recombinant HCV core polypeptides and recombinant Treponema pallidum 47 kDa antigen polypeptides contg. hepatitis B virus HBc protein-derived **nucleic acid** binding motif were prepd. for the disclosed immunoassay. Recombinant HCV core polypeptide contg. mouse protamine 1-derived **nucleic acid**-binding motif was also prepd. in the invention.

ST **nucleic acid bound polypeptide** immunoassay; antibody antigen **nucleic acid** bound immunoassay

IT Protamines
RL: ARU (Analytical role, unclassified); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(1, **nucleic acid**-binding motif; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT Proteins (specific proteins and subclasses)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(47,000-mol.-wt.; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT Hepatitis B virus
(HBc protein **nucleic acid**-binding motif; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT Peptides, analysis
RL: ARU (Analytical role, unclassified); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(**nucleic acid**-binding motif; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT Treponema pallidum
(**nucleic acid**-bound 47 kDa antigen; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT Fusion proteins (chimeric proteins)
Hepatitis C core antigen
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(**nucleic acid**-bound; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT Agglutination test
DNA sequences
Genetic engineering
Hepatitis C virus
Immunoassay
Protein sequences

cDNA sequences
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT Antigens
RL: ANT (Analyte); ARG (Analytical reagent use); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT Antibodies
RL: ANT (Analyte); ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT Proteins (general), biological studies
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT Hepatitis B core antigen
RL: ARU (Analytical role, unclassified); BPN (Biosynthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT **Nucleic acids**
RL: ARU (Analytical role, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT Chimeric genes
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT 117501-43-6, Protamine 1 (mouse precursor reduced) 199489-22-0 199489-24-2 199489-26-4 199489-28-6 199489-30-0
RL: PRP (Properties)
(amino acid sequence; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT 94569-29-6, DNA (mouse protamine 1 cDNA) 199489-21-9 199489-23-1 199489-25-3 199489-27-5 199489-29-7
RL: PRP (Properties)
(nucleotide sequence; prepn. of **nucleic acid-bound polypeptides** for immunoassay of antigen or antibody)

IT 199488-16-9P, DNA (synthetic 102-nucleotide fragment)
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

IT 199542-68-2
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(prepn. of **nucleic acid-bound** **polypeptides** for immunoassay of antigen or antibody)

L7 ANSWER 2 OF 8 MEDLINE
AN 1998022896 MEDLINE
DN 98022896
TI The N tails of histones H3 and H4 adopt a highly structured conformation

in the nucleosome.
AU Ban`eres J L; Martin A; Parello J
CS UPRESA CNRS 5074, Chimie Biomoleculaire et Interactions Biologiques, Faculte de Pharmacie, 34060 Montpellier, Cedex 2, France.
SO JOURNAL OF MOLECULAR BIOLOGY, (1997 Oct 31) 273 (3) 503-8. Journal code: J6V. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199803
EW 19980304
AB The histone N tails correspond to conserved amino acid sequences that are peripherally located in the nucleosome and undergo a variety of post-synthetic modifications during cell cycle. These N tails have been recently recognized as directly interacting with transcription-related proteins. We show here, based on circular dichroic evidence, that the N tails of both tetrameric histones H3 and H4 are highly organized as DNA-**bound polypeptide** segments in the nucleosome core particle, with about half of their residues, taken together, being alpha-helical. In contrast, the N tails of both dimeric histones H2A and H2B are found essentially in a random-coil conformation. The implications of these findings on nucleosome structure and recognition are discussed. Copyright 1997 Academic Press Limited.
CT Check Tags: Animal; Support, Non-U.S. Gov't
Binding Sites
Circular Dichroism
Cysteine Proteinases: ME, metabolism
DNA: CH, chemistry
DNA: ME, metabolism
*Histones: CH, chemistry
Histones: ME, metabolism
Nucleic Acid Conformation
*Nucleosomes: CH, chemistry
*Protein Conformation
Rats
Trypsin: ME, metabolism
RN 9007-49-2 (DNA)
CN EC 3.4.21.4 (Trypsin); EC 3.4.22 (Cysteine Proteinases); EC 3.4.22.8 (clostripain); 0 (Histones); 0 (Nucleosomes)

L7 ANSWER 3 OF 8 MEDLINE
AN 96199185 MEDLINE
DN 96199185
TI A conserved HPD sequence of the J-domain is necessary for YDJ1 stimulation of Hsp70 ATPase activity at a site distinct from substrate binding.
AU Tsai J; Douglas M G
CS Department of Biochemistry and Biophysics, School of Medicine, University of North Carolina at Chapel Hill 27599, USA.
NC 5-RO1-AG11527-01-03 (NIA)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Apr 19) 271 (16) 9347-54. Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199608
AB The 46-kDa protein YDJ1 is one of several known yeast homologues of the Escherichia coli DnaJ protein. Like all J homologues, it shares homology with the highly conserved NH2-terminal "J-domain" of DnaJ. A component of

the DnaK (Hsp70) chaperone machinery that mediates protein folding, DnaJ is necessary for survival at elevated temperatures. It stimulates ATP hydrolysis by DnaK and effects the release of DnaK-**bound polypeptides**. Previous genetic and biochemical studies indicate that the J-domain is necessary for these functions. Using peptides corresponding to J-domain sequence, we show that a peptide containing the highly conserved His-Pro-Asp sequence at positions 34-36 in the J-domain competes off YDJ1 stimulation of Hsp70 ATPase activity. Inhibitory concentrations of peptide do not prevent binding of folding substrates, therefore YDJ1 must interact with Hsp70 at a site distinct from that for substrate binding. This interaction is critical for Hsp70 activity, since a mutant YDJ1 protein harboring a H34Q change (ydj1Q34) stimulates neither Hsp70 ATPase nor substrate release. The importance of the proper function of this region of the protein is supported by the poor growth and temperature-sensitive phenotype of yeast expressing ydj1Q34.

CT Check Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
*Adenosinetriphosphatase: ME, metabolism
Amino Acid Sequence
Binding Sites
Conserved Sequence
DNA Primers
Escherichia coli: ME, metabolism
*Fungal Proteins: CH, chemistry
*Fungal Proteins: ME, metabolism
Heat-Shock Proteins: CH, chemistry
Heat-Shock Proteins: ME, metabolism
*Heat-Shock Proteins 70: ME, metabolism
Kinetics
Molecular Sequence Data
Mutagenesis, Site-Directed
Point Mutation
Polymerase Chain Reaction
Repetitive Sequences, Nucleic Acid
*Saccharomyces cerevisiae: ME, metabolism

RN 139874-78-5 (YDJ1 protein)

CN EC 3.6.1.3 (Adenosinetriphosphatase); 0 (DNA Primers); 0 (DNAS protein); 0 (Fungal Proteins); 0 (Heat-Shock Proteins 70); 0 (Heat-Shock Proteins)

L7 ANSWER 4 OF 8 WPIDS COPYRIGHT 1999 DERWENT INFORMATION LTD

AN 1994-341880 [42] WPIDS

DNC C1994-155803

TI Efficient cell free protein synthesis using purified ribosome fraction - in a transcription-translation medium, opt. contg. chaperone proteins.

DC B04 D16

IN HARDESTY, B; KRAMER, G; KUDLICKI, W

PA (RERE-N) RES DEV FOUND

CYC 28

PI WO 9424303 A1 19941027 (199442)* EN 54p C12P021-00
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE
W: AU CA CN FI JP KR NO NZ RU US
AU 9466288 A 19941108 (199507) C12P021-00
ZA 9402335 A 19951129 (199601) 116p A61K000-00
EP 693131 A1 19960124 (199609) EN C12P021-00
R: AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL PT SE
NZ 265504 A 19960925 (199644) C12P021-00
JP 08508651 W 19960917 (199704) 47p C12N015-09
AU 693443 B 19980702 (199837) C12P021-00

ADT WO 9424303 A1 WO 1994-US3860 19940408; AU 9466288 A AU 1994-66288 19940408; ZA 9402335 A ZA 1994-2335 19940407; EP 693131 A1 EP 1994-914083

19940408, WO 1994-US3860 19940408; NZ 265504 A NZ 1994-265504 19940408, WO
1994-US3860 19940408; JP 08508651 W JP 1994-523319 19940408, WO
1994-US3860 19940408; AU 693443 B AU 1994-66288 19940408
FDT AU 9466288 A Based on WO 9424303; EP 693131 A1 Based on WO 9424303; NZ
265504 A Based on WO 9424303; JP 08508651 W Based on WO 9424303; AU 693443
B Previous Publ. AU 9466288, Based on WO 9424303
PRAI US 1993-45445 19930408; US 1994-219971 19940404
REP 05Jnl.Ref
IC ICM A61K000-00; C12N015-09; C12P021-00
ICS C12P021-02
AB WO 9424303 A UPAB: 19941212
Highly efficient cell free protein synthesis comprises (1) prepn. of a cell free extract; (2) sepn. of a ribosome fraction (RF), practically free of soluble enzyme that degrade protein and **nucleic acids**; (3) incubating RF in a transcription/translation medium and (4) measuring the amt. of protein synthesised. The incubation system may include chaperone proteins.

ADVANTAGE - This method is a very efficient system for engineering and synthesis of prokaryotic or eukaryotic proteins. Purified RF is (1) free of soluble components that may complicate purificn. and analysis (and possibly also interfere with translation/transcription); (2) is less viscous, and (3) reduces turbidity (and thus clogging in continuous flow systems. The use of a circular plasmid as DNA source provides a more stable transcription system and tRNA with modified (e.g. fluorophore labelled) amino acids can be used. CP promote release and activation of ribosome **bound polypeptides**.

Dwg.0/5
FS CPI
FA AB; GI
MC CPI: B04-N04; D05-C12; D05-H01; D05-H17A; D05-H19

L7 ANSWER 5 OF 8 EMBASE COPYRIGHT 1999 ELSEVIER SCI. B.V.
AN 91147017 EMBASE
DN 1991147017
TI rRNA binding domain of yeast ribosomal protein L25. Identification of its borders and a key leucine residue.
AU Rutgers C.A.; Rientjes J.M.J.; Van 't Riet J.; Raue H.A.
CS Biochemisch Laboratorium, Vrije Universiteit, De Boelelaan 1083,1081 HV Amsterdam, Netherlands
SO Journal of Molecular Biology, (1991) 218/2 (375-385).
ISSN: 0022-2836 CODEN: JMOBAK
CY United Kingdom
DT Journal; Article
FS 004 Microbiology
LA English
SL English
AB We have delineated the region of yeast ribosomal protein L25 responsible for its specific binding to 26 S rRNA by a novel approach using in vitro synthesized, [35S]methionine-labeled fragments as well as point mutants of the L25 protein. The rRNA binding capacity of these mutants polypeptides was tested by incubation with an in vitro transcribed, biotinylated fragment of yeast 26 S rRNA that contains the complete L25 binding site. Protein-rRNA interaction was assayed by binding of the rRNA-r-protein complex to streptavidin-agarose followed either by analysis of the **bound polypeptide** by SDS/polyacrylamide gel electrophoresis or by precipitation with trichloroacetic acid. Our results

show that the structural elements necessary and sufficient for specific interaction of L25 with 26 S rRNA are contained in the region bordered by amino acids 62 and 126. The remaining parts of the protein, in particular the C-terminal 16 residues, while not essential for binding, do enhance its affinity for 26 S rRNA. To test whether, as suggested by the results of the deletion experiments, the evolutionarily conserved sequence motif K120KAYVRL126 is involved in rRNA binding, we replaced the leucine residue at position 126 by either isoleucine or lysine. The first substitution did not affect binding. The second, however, completely abolished the specific rRNA binding capacity of the protein. Thus, Leu126, and possibly the whole conserved sequence motif, plays a key role in binding of L25 to 26 S rRNA.

CT Medical Descriptors:
article
binding site
nonhuman
priority journal
protein nucleic acid interaction
yeast
Drug Descriptors:
*rna
*ribosome protein
*ribosome rna

RN (rna) 63231-63-0

L7 ANSWER 6 OF 8 MEDLINE
AN 92038932 MEDLINE
DN 92038932
TI Nucleotide sequence of the ethidium efflux gene from Escherichia coli.
AU Purewal A S
CS Department of Veterinary Pathology, Royal Veterinary College, London, U.K..
SO FEMS MICROBIOLOGY LETTERS, (1991 Aug 1) 66 (2) 229-31.
Journal code: FML. ISSN: 0378-1097.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-S63865; GENBANK-S76128; GENBANK-S70107; GENBANK-S70109; GENBANK-S70115; GENBANK-S70117; GENBANK-S70121; GENBANK-S70125; GENBANK-S70128; GENBANK-S70130
EM 199202
AB The nucleotide sequence of the gene specifying the ethidium efflux system of Escherichia coli has been determined. The translated open reading frame has identified a membrane-**bound polypeptide** of 110 amino acids (11,960 Da) which shares 42% identity with a staphylococcal protein specifying resistance to ethidium.

CT Amino Acid Sequence
*Bacterial Proteins: GE, genetics
Base Sequence
*Drug Resistance: GE, genetics
*Escherichia coli: GE, genetics
Escherichia coli: ME, metabolism
Ethidium: ME, metabolism
*Ethidium: PD, pharmacology
*Membrane Proteins: GE, genetics

Molecular Sequence Data
Open Reading Frames: GE, genetics
Plasmids: GE, genetics
Sequence Homology, Nucleic Acid
Staphylococcus aureus: GE, genetics
RN 3546-21-2 (Ethidium)
CN 0 (Bacterial Proteins); 0 (Membrane Proteins); 0 (Plasmids)
GEN EBR

L7 ANSWER 7 OF 8 MEDLINE DUPLICATE 2
AN 85261408 MEDLINE
DN 85261408
TI Hybridization selection of covalent **nucleic acid**-protein complexes. 2. Cross-linking of proteins to specific Escherichia coli mRNAs and DNA sequences by formaldehyde treatment of intact cells.
AU Schouten J P
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1985 Aug 15) 260 (17) 9929-35. Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 198511
AB Proteins cross-linked to pBR322 mRNAs and DNA by formaldehyde treatment of intact Escherichia coli cells have been detected with the use of a novel detection method. Among the proteins cross-linked to pBR322 mRNAs were S1, S21, and at least six other proteins of the small ribosomal subunit, initiation factor 1, elongation factor (EF) Tu, and very small amounts of EF-G and EF-Ts. The single strand binding protein, the HU-proteins, and RNA polymerase subunits alpha and beta were among the proteins cross-linked to pBR322 DNA. The results obtained suggest that the procedures described, can also be used to study interactions between different **nucleic acid-bound polypeptides**. The results are discussed in relation to the working mechanism of formaldehyde, and are compared to the results obtained with cross-linking induced by ultraviolet light. The methods presented should also be of use for the study of **nucleic acid**-protein interactions in other organisms.
CT Bacterial Proteins: ME, metabolism
Chromatography, Affinity
DNA-Binding Proteins: ME, metabolism
DNA-Directed RNA Polymerase: ME, metabolism
*DNA, Bacterial: ME, metabolism
Escherichia coli: DE, drug effects
*Escherichia coli: GE, genetics
*Formaldehyde: PD, pharmacology
Molecular Weight
Peptide Elongation Factors: ME, metabolism
*Proteins: ME, metabolism
Ribosomal Proteins: ME, metabolism
*RNA, Messenger: ME, metabolism
RN 50-00-0 (Formaldehyde)
CN EC 2.7.7.6 (DNA-Directed RNA Polymerase); 0 (elongation factor G); 0 (eIF-1); 0 (Bacterial Proteins); 0 (DNA-Binding Proteins); 0 (DNA, Bacterial); 0 (Peptide Elongation Factor Tu); 0 (Peptide Elongation Factors); 0 (Ribosomal Proteins); 0 (RNA, Messenger)

L7 ANSWER 8 OF 8 CAPLUS COPYRIGHT 1999 ACS
AN 1968:112996 CAPLUS

DN 68:112996
TI Chemical identification of specific immunoglobulins as the product of a cell-free system from plasmocytoma tumors
AU Mach, Bernard; Koblet, Hans; Gros, Denise
CS Univ. Geneva, Geneva, Switz.
SO Proc. Natl. Acad. Sci. U. S. A. (1968), 59(2), 445-52
CODEN: PNASA6
DT Journal
LA English
CC 13 (Immunochemistry)
AB A plasmocytoma cell-free system highly active in cell-free protein synthesis was defined. In order to identify amino acid sequences that were specific to a given immunoglobulin mol., a chem. anal. by electrophoresis and chromatog. of the tryptic peptides of the product were made, including all unfinished microsome-**bound** **polypeptide** chains. With 2 different plasmocytoma tumors, the specific peptides of a given immunoglobulin were synthesized in the cell-free system and were characterized chem. The chem. anal. of the cell-free product provided an exptl. test for the possible role of sol. RNA or activating enzyme in the control of immunoglobulin variability.
ST SEQUENCES IMMUNOGLOBULINS; TUMOR IMMUNOGLOBULINS; PEPTIDES IMMUNOGLOBULINS; IMMUNOGLOBULINS PLASMOCYTOMA; PLASMOCYTOMA IMMUNOGLOBULINS
IT Globulins, immune
RL: FORM (Formation, nonpreparative)
(formation of, by plasmocytoma cell-free system, variation of)
IT Myeloma
(immune globulin formation by cell-free system of plasma-cell)
IT **Nucleic acids**, ribo-, transfer
RL: BIOL (Biological study)
(in immune globulin formation by plasmacytoma)

L8 28 FILE MEDLINE
L9 38 FILE CAPLUS
L10 25 FILE BIOSIS
L11 26 FILE EMBASE
L12 3 FILE WPIDS

TOTAL FOR ALL FILES
L13 120 NUCLEIC ACID BIND? MOTIF?

=> s l13 and (amino acid sequence or immunoassay)

L14 23 FILE MEDLINE
L15 21 FILE CAPLUS
L16 15 FILE BIOSIS
L17 6 FILE EMBASE
L18 0 FILE WPIDS

TOTAL FOR ALL FILES
L19 65 L13 AND (AMINO ACID SEQUENCE OR IMMUNOASSAY)

=> s genetic engineer? and l19

L20 0 FILE MEDLINE
L21 1 FILE CAPLUS
L22 0 FILE BIOSIS
L23 0 FILE EMBASE
L24 0 FILE WPIDS

TOTAL FOR ALL FILES
L25 1 GENETIC ENGINEER? AND L19

=> d cbib abs

L25 ANSWER 1 OF 1 CAPLUS COPYRIGHT 1999 ACS
1997:732139 Document No. 128:32121 Nucleic acid-bound polypeptide, method of
producing nucleic acid-bound polypeptide, and **immunoassay** using
the polypeptide. Takemura, Fuminori; Ueno, Eiichi; Itoh, Satoru
(Fujirebio Inc., Japan). Eur. Pat. Appl. EP 805160 A1 19971105, 38 pp.
DESIGNATED STATES: R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL,
SE, MC, PT, IE, FI. (English). CODEN: EPXXDW. APPLICATION: EP
1997-400985 19970430. PRIORITY: JP 1996-134444 19960501.
AB A nucleic acid-bound polypeptide produced by binding a nucleic acid to a
polypeptide, a method of producing the nucleic acid-bound polypeptide, and
applications of the nucleic acid-bound polypeptide, including
immunoassays for an antigen or antibody, such as an agglutination
immunoassay are provided. Recombinant HCV core polypeptides and
recombinant Treponema pallidum 47 kDa antigen polypeptides contg.
hepatitis B virus HBc protein-derived **nucleic acid**
binding motif were prepd. for the disclosed
immunoassay. Recombinant HCV core polypeptide contg. mouse
protamine 1-derived **nucleic acid-binding**
motif was also prepd. in the invention.

=> s agglutin? and immunoassay and nucleic acid and (bind? or bound?)(w)motif

L26 0 FILE MEDLINE
L27 1 FILE CAPLUS
L28 0 FILE BIOSIS
L29 0 FILE EMBASE
L30 0 FILE WPIDS

TOTAL FOR ALL FILES
L31 1 AGGLUTIN? AND IMMUNOASSAY AND NUCLEIC ACID AND (BIND? OR BOUND?)
(W) MOTIF

=> s l31 not l25

L32 0 FILE MEDLINE
L33 0 FILE CAPLUS
L34 0 FILE BIOSIS
L35 0 FILE EMBASE
L36 0 FILE WPIDS

TOTAL FOR ALL FILES
L37 0 L31 NOT L25

=> s takemura f?/au,in;s ueno e?/au,in

'IN' IS NOT A VALID FIELD CODE
L38 9 FILE MEDLINE
L39 86 FILE CAPLUS
L40 11 FILE BIOSIS
'IN' IS NOT A VALID FIELD CODE

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L41           9 FILE EMBASE
L42           7 FILE WPIDS

TOTAL FOR ALL FILES
L43         122 TAKEMURA F?/AU,IN


'IN' IS NOT A VALID FIELD CODE
L44          79 FILE MEDLINE
L45          83 FILE CAPLUS
L46          88 FILE BIOSIS
'IN' IS NOT A VALID FIELD CODE
L47          73 FILE EMBASE
L48          18 FILE WPIDS

TOTAL FOR ALL FILES
L49         341 UENO E?/AU,IN

=> s 143 and 149

L50           0 FILE MEDLINE
L51           1 FILE CAPLUS
L52           0 FILE BIOSIS
L53           0 FILE EMBASE
L54           1 FILE WPIDS

TOTAL FOR ALL FILES
L55           2 L43 AND L49

=> s 155 not 125

L56           0 FILE MEDLINE
L57           0 FILE CAPLUS
L58           0 FILE BIOSIS
L59           0 FILE EMBASE
L60           1 FILE WPIDS

TOTAL FOR ALL FILES
L61           1 L55 NOT L25

=> d


L61  ANSWER 1 OF 1  WPIDS COPYRIGHT 1999   DERWENT INFORMATION LTD
AN   1997-529030 [49]   WPIDS
DNN  N1997-440669       DNC C1997-168434
TI   Nucleic acid-bound polypeptide - useful as immunoassay reagent.
DC   B04 D16 S03
IN   ITOH, S; TAKEMURA, F; UENO, E
PA   (FJRE) FUJIREBIO INC; (FJRE) FUJIREBIO KK
CYC  20
PI   EP 805160     A1 19971105 (199749)* EN   38p    C07K002-00
         R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
     AU 9719978    A  19971204 (199806)             C12N015-62
     JP 10081698   A  19980331 (199823)       20p   C07K001-113
ADT  EP 805160 A1 EP 1997-400985 19970430; AU 9719978 A AU 1997-19978
19970430;
     JP 10081698 A JP 1997-121803 19970424
PRAI JP 1996-134444   19960501
IC   ICM  C07K001-113; C07K002-00; C12N015-62
     ICS  C07K001-14; C07K017-06; C07K019-00; C12N015-09; C12P021-02;
```